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The vertebrate retina sequentially transforms patterns of neural activity through 5 separate, serially arranged sheets of cells. These neuronal patterns become increasingly complex at each successive layer. Our objectives is to determine the parameters in space and time for the transfer functions that transform the patterns at successive layers. We have extracted the space and time constants for retinal processing from the physiological data taken from single cells at each retinal layer. These space-time parameters drive an image processing computer, the PIPE. The resulting program represents a tentative blueprint for design of a retina, and some of these values have been used by modelers to make artificial retinas, including the silicon retina developed by Misha Mahawold in Carver Mead's laboratory.

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Remarks: Here is another copy of the interim report (Technical) that was sent to your office last July (apparently, it was misplaced).

PROGRESS REPORT
AFOSR-91-0196

INTRODUCTION

The vertebrate retina sequentially transforms patterns of neural activity through 5 separate, serially arranged sheets of cells. These neuronal patterns become increasingly complex at each successive layer. Our objective is to determine the parameters in space and time for the transfer functions that transform the patterns at successive layers. We have extracted the space and time constants for retinal processing from the physiological data taken from single cells at each retinal layer. These space-time parameters drive an image processing computer, the PIPE. The resulting program represents a tentative blueprint for design of a retina, and some of these values have been used by modelers to make artificial retinas, including the silicon retina developed by Misha Mahawold in Carver Mead's laboratory.

QUESTIONS ADDRESSED DURING THE FIRST YEAR

To what extent are the parameters we've selected accurate and complete? To answer these questions we programmed an image processing computer, the PIPE, to generate images that represent the patterns of activity at each retinal level; creating a computer-based dynamic model of retinal function. The emergent patterns are the results of a first attempt to generate a complete representation of the dynamic forms of retinal function at all retinal levels. We will now compare the images generated by the compute with those images generated directly by the retina itself.

RESULTS OF STUDIES DURING THE FIRST YEAR

At the start of the current grant period we developed a methodology for measuring and evaluating the patterns actually derived from the physiological experiments, within each of the retinal sheets. With the actual physiological patterns we could begin to evaluate the parameters programmed into the PIPE by comparing the measurements of patterns derived physiologically from the retina with those generated by the PIPE.

The physiological method we use involves recording intracellularly from each of the single representative cell-types at each retina level. As one moves through the retina one encounters increasing numbers of different cell types at each level. For example, there are at least two photoreceptor types, 4 different bipolar cell types, and up to 8 different ganglion cell types. Each study covers one type at a time.

When the cell is acquired we run a set of about 100 sequential trials stimulating the cell with a stimulus pattern at 100 different positions with respect to the cell. This is equivalent to recording sequentially from 100 cells of that type at different positions with respect to the pattern. We then reassemble the data from the 100 trials to display the patterns of neural activity generated as the simultaneous responses of this population of cells to the stimulus pattern.

The advantage of the method is that we have information about both the excitatory and inhibitory components (these are intracellular recordings) of responses from the population of each cell type, and we can perform these studies at every level of the retina on every cell type. (Compare this with the alterative method of recording simultaneously with an electrode array. There one only has access to the ganglion cells, and one can only record the result of excitatory and inhibitory influences on the cell).

METHODS DEVELOPED DURING THE CURRENT YEAR

To perform these studies we have built a special physiological setup that allows us to measure activity in an intact retina at each retinal level. We have also developed the computer software to stimulate the retina with a variety of patterns and at the same time keeping track of the position of the stimulus so that we can reassemble the data when the experimental runs are completed.

We have begun these studies at the ganglion cell level because ganglion cells represent a culmination of all retinal cell processing. It is at the ganglion cell level that all more distal retinal interactions are expressed.

So far our data has shown that the output patterns recorded from the live retina resemble closely the patterns predicted by the PIPE. There are, however, some interesting differences. The predicted ganglion cell output is almost always overshadowed by the inhibitory activity of the change-sensitive amacrine cells. The measured physiological output, however, appears to be less overshadowed and therefore more robust. The discrepancy is probably due to an error in our estimate of the strength and/or timing of the amacrine cell system.

This discrepancy brings up an important point about the underlying philosophy of the project. As physiologists we are used to thinking about signal processing in neural systems in terms of cellular activity. But in the design of a model, we must begin to think more in terms of interactions of cellular networks. There is no way to directly measure the influence of one cellular network upon another, so in building the model we must estimate the magnitude of the interactions based upon intracellular measurements. For example, every recorded ganglion cell is influenced by the wide spread action of the amacrine cell network, so we modeled the interaction by allowing ganglion cells to be inhibited by the amacrine cells. By comparing the modeled with the measured network activity, we can determine the values of amacrine cell network action on the ganglion cells.

OBJECTIVES FOR THE UPCOMING YEAR

1. During the upcoming year we will measure patterns at each retina level and compare these with those generated by the PIPE.
2. We will also record "intracellularly" from each pixel to correlate the quantitative details of computer function with those of single cell activity. These studies will give us the exact time course of response at each point in retinal space, to compare with the signals generated by the PIPE.
3. We will generate a full set of parameters for specifying retinal function based upon known retinal anatomy. Figure 1 shows the full set of 17 parameters that needs to be specified for retinal function. We have begun to catalog these values. For those parameters that are unknown, we will make the appropriate measurements. For those parameters that are unmeasurable, we will compare measured and predicted patterns and adjust values to achieve minimal differences.

We will set up the PIPE so that we can vary these parameters at will to generate visual function in retinas other than that of the salamander. It will be interesting, for example, to look at the details of cat and monkey vision, using a standard visual processing paradigm.

OBJECTIVES FOR FUTURE YEARS IF FUNDING CONTINUES

We have begun discussions with other laboratories to collaborate and generate parameter sets for the retinas of other animals.

3. Collaborate with Bob Shapley on parameters from monkey retina
4. Collaborate with Ralph Nelson (NIH) on parameters for cat

These studies will generate both real and simulated patterns of activity for cat and monkey retinal vision.

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